

## SEQUENCE LISTING

<110> KYOWA HAKKO KOGYO CO., LTD

<120> An agent for prevention and/or treatment of itching

<130> 11503W01

<140>

<141>

<150> JP 2002/241522

<151> 2002-08-22

<160> 20

<170> PatentIn Ver. 2.1

<210> 1

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 1

tcgacaaata aagcaatagc atcacaaatt tcacaaataa agcatttttt tcaa

54

<210> 2

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 2

tgcatgtgaaa aaaatgcctt atttgtgaaa ttgtgatgc tattgcttta ttig 54

<210> 3

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 3

tgcatcttag ttgtggtttg tccaaactcg agccccggg 39

<210> 4

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 4

gtacccccgg gctcgagttt ggacaaacca caactagaa 39

<210> 5

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 5

tcgacgggtat cgattcgact gacgtcatac ttgacgtcac

40

<210> 6

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 6

tcgagtgacg tcaagtatga cgtcagtcga atcgataccg

40

<210> 7

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 7

gccccagaag cttaagtgcc caccatggg

29

<210> 8

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 8

gttcattgtg gcggccgcag catcttcagc tgc

33

<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 9

cggagacict agagggtata taatg

25

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 10

ctaatacgac tcactatagg g

21

<210> 11

<211> 362

<212> PRT

<213> Homo sapiens

<400> 11

Met Gly Asn His Thr Trp Glu Gly Cys His Val Asp Ser Arg Val Asp  
1 5 10 15

His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val Gly Leu  
20 25 30

Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln  
35 40 45

Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu  
50 55 60

Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His  
65 70 75 80

Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile  
85 90 95

Phe Tyr Thr Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys Ile Ser  
100 105 110

Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala Arg Leu  
115 120 125

Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp Ala Thr  
130 135 140

Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu Phe Arg  
145 150 155 160

Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met Glu Gly  
165 170 175

Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe Leu Phe  
180 185 190

Pro Trp Ala Leu Met Leu Leu Ser Tyr Arg Gly Ile Leu Arg Ala Val  
195 200 205

Arg Gly Ser Val Ser Thr Glu Arg Gln Glu Lys Ala Lys Ile Lys Arg  
210 215 220

Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala Pro Tyr  
225 230 235 240

His Val Leu Leu Leu Ser Arg Ser Ala Ile Tyr Leu Gly Arg Pro Trp  
245 250 255

Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser Ser Leu  
260 265 270

Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Leu  
275 280 285

Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His Asn Leu  
290 295 300

Leu Arg Phe Leu Ala Ser Asp Lys Pro Gln Glu Met Ala Asn Ala Ser  
305 310 315 320

Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Asn Ser Thr Ala Lys  
325 330 335

Ala Met Thr Gly Ser Trp Ala Ala Thr Pro Pro Ser Gln Gly Asp Gln  
340 345 350

Val Gln Leu Lys Met Leu Pro Pro Ala Gln  
355 360

<210> 12  
 <211> 2932  
 <212> DNA  
 <213> Homo sapiens

<400> 12

ctgcagtcag gcggatgaact gacitcatcc caatccctca gccccacca ggaccagtc	60
ggagtcctc cctgcccc attgaaattt ccttcctgc ccaaactta cctctgact	120
agaccttact cactccttc cgttttcta agatccttc ctgccgtcca cagaccgagc	180
cttttatctt tgtccacct gtgccagaca cctcctttc cagaaccttc tctttactgg	240
tgaccttact tatctctgtt gctttctggg gtcctaggaa atgccagcac tcccaccac	300
attgccigaa ctttccaaca ctccctagct gcgctgtgtc ctatctcaac acttctcat	360
gtatttcttg tgtcttctag aacattcccc cgccattatt acttcaatat ggctacacat	420
acttctaat tgccttgcaa accatctctt tctcaccatt gccagcgat gctttcgtct	480
cctccataaa cactcccgga gaccaatttt tgtgtcacc ccatactccc tctttgacac	540
actgactcca tacataacct ccttgaaaaa cctctttatt aatctacca tctccagac	600
tctctctctg tcataattcc atccctcttc caacttttc ctctcaagct ctgcccttc	660
cagcccagcc cagcctaccc aacctcatct ctccctgta gaccacatcc caccatgttc	720
ccctgagcct ccaaggaagg ggctcagggg gcccattggc ctcccgctcc ctgtggcccc	780
acagcccccg tgggccaggg gaagcgcccc agaagccgaa gtgcccacc atg ggc aac	838

Met Gly Asn

1

cac acg tgg gag ggc tgc cac gtg gac tgc cgc gtg gac cac ctc ttt	886
His Thr Trp Glu Gly Cys His Val Asp Ser Arg Val Asp His Leu Phe	

5

10

15

ccg cca tcc ctc tac atc ttt gtc atc ggc gtg ggg ctg ccc acc aac	934
Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val Gly Leu Pro Thr Asn	

20

25

30

35

tgc ctg gct ctg tgg gcg gcc tac cgc cag gtg caa cag cgc aac gag	982
Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val Gln Gln Arg Asn Glu	

40

45

50

ctg ggc gtc tac ctg atg aac ctc agc atc gcc gac ctg ctg tac atc 1030  
 Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala Asp Leu Leu Tyr Ile  
                   55                                  60                                  65

tgc acg ctg ccg ctg tgg gtg gac tac ttc ctg cac cac gac aac tgg 1078  
 Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu His His Asp Asn Trp  
                   70                                  75                                  80

atc cac ggc ccc ggg tcc tgc aag ctc ttt ggg ttc atc ttc tac acc 1126  
 Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly Phe Ile Phe Tyr Thr  
                   85                                  90                                  95

aat atc tac atc agc atc gcc ttc ctg tgc tgc atc tgc gtg gac cgc 1174  
 Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys Ile Ser Val Asp Arg  
 100                                  105                                  110                                  115

tac ctg gct gtg gcc cac cca ctc cgc ttc gcc cgc ctg cgc cgc gtc 1222  
 Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala Arg Leu Arg Arg Val  
                   120                                  125                                  130

aag acc gcc gtg gcc gtg agc tcc gtg gtc tgg gcc acg gag ctg ggc 1270  
 Lys Thr Ala Val Ala Val Ser Ser Val Val Trp Ala Thr Glu Leu Gly  
                   135                                  140                                  145

gcc aac tgc gcg ccc ctg ttc cat gac gag ctc ttc cga gac cgc tac 1318  
 Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu Phe Arg Asp Arg Tyr  
                   150                                  155                                  160

aac cac acc ttc tgc ttt gag aag ttc ccc atg gaa ggc tgg gtg gcc 1366  
 Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met Glu Gly Trp Val Ala  
                   165                                  170                                  175

tgg atg aac ctc tat cgg gtg ttc gtg ggc ttc ctc ttc ccg tgg gcg 1414  
 Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe Leu Phe Pro Trp Ala  
 180                                  185                                  190                                  195



ctc atg ctg ctg tgc tac cgg ggc atc ctg cgg gcc gtg cgg ggc agc 1462  
 Leu Met Leu Leu Ser Tyr Arg Gly Ile Leu Arg Ala Val Arg Gly Ser  
                     200                    205                    210

gtg tcc acc gag cgc cag gag aag gcc aag atc aag cgg ctg gcc ctc 1510  
 Val Ser Thr Glu Arg Gln Glu Lys Ala Lys Ile Lys Arg Leu Ala Leu  
                     215                    220                    225

agc ctc atc gcc atc gtg ctg gtc tgc ttt gcg ccc tat cac gtg ctc 1558  
 Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala Pro Tyr His Val Leu  
                     230                    235                    240

ttg ctg tcc cgc agc gcc atc tac ctg ggc cgc ccc tgg gac tgc ggc 1606  
 Leu Leu Ser Arg Ser Ala Ile Tyr Leu Gly Arg Pro Trp Asp Cys Gly  
                     245                    250                    255

ttc gag gag cgc gtc ttt tct gca tac cac agc tca ctg gct ttc acc 1654  
 Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser Ser Leu Ala Phe Thr  
 260                    265                    270                    275

agc ctc aac tgt gtg gcg gac ccc atc ctc tac tgc ctg gtc aac gag 1702  
 Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr Cys Leu Val Asn Glu  
                     280                    285                    290

ggc gcc cgc agc gat gtg gcc aag gcc ctg cac aac ctg ctc cgc ttt 1750  
 Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His Asn Leu Leu Arg Phe  
                     295                    300                    305

ctg gcc agc gac aag ccc cag gag atg gcc aat gcc tgc ctc acc ctg 1798  
 Leu Ala Ser Asp Lys Pro Gln Glu Met Ala Asn Ala Ser Leu Thr Leu  
                     310                    315                    320

gag acc cca ctc acc tcc aag agg aac agc aca gcc aaa gcc atg act 1846  
 Glu Thr Pro Leu Thr Ser Lys Arg Asn Ser Thr Ala Lys Ala Met Thr  
                     325                    330                    335



Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val  
20 25 30

Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val  
35 40 45

Arg Gln His Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala  
50 55 60

Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu  
65 70 75 80

His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly  
85 90 95

Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys  
100 105 110

Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala  
115 120 125

Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp  
130 135 140

Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu  
145 150 155 160

Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met  
165 170 175

Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe  
180 185 190

Leu Phe Pro Trp Ala Leu Met Leu Leu Cys Tyr Arg Gly Ile Leu Arg  
195 200 205

Ala Val Gln Ser Ser Val Ser Thr Glu Arg Gln Glu Lys Val Lys Ile  
210 215 220

Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala  
225 230 235 240

Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg  
245 250 255

Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser  
260 265 270

Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr  
275 280 285

Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His  
290 295 300

Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn  
305 310 315 320

Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr  
325 330 335

Gly Lys Ser Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly  
340 345 350

Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln  
355 360 365

<210> 14

<211> 1098

<212> DNA

<213> Mus musculus

<400> 14

atg gac aac agc acg ggc aca ggg gag ggc tgc cat gtg gac tct cga	48
Met Asp Asn Ser Thr Gly Thr Gly Glu Gly Cys His Val Asp Ser Arg	
1 5 10 15	
gtg gac cac ctc ttc cca cca tct ctc tac atc ttc gtc atc ggg gtg	96
Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val	
20 25 30	
ggg ctg ccc acc aac tgc ctg gcc ctg tgg gca gcc tac cgg cag gtg	144
Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val	
35 40 45	
cgc caa cac aat gag ctg ggc gtc tac ctg atg aac ttg agc att gca	192
Arg Gln His Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala	
50 55 60	
gac ctg ctg tac atc tgc act ttg ccg ctg tgg gtc gac tac ttc ctc	240
Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu	
65 70 75 80	
cac cat gac aac tgg atc cac ggc cct ggc tcc tgc aag ctc ttt ggc	288
His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly	
85 90 95	
ttc atc ttc tac agc aac atc tat atc agc atc gcc ttc ctg tgc tgc	336
Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys	
100 105 110	
atc tcc gtg gac cgc tac ctg gct gtg gct cat cct ctg cgc ttt gca	384
Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala	
115 120 125	
cgc ctg cgc cgg gtc aag aca gca gtg gct gtg agc tct gtg gtc tgg	432
Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp	

130	135	140	
gcc acg gag ctg ggc gcc aat tca gca ccg ctc ttc cat gat gag ctg			480
Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu			
145	150	155	160
tti cgt gat cgc tac aac cac acc ttc tgc ttt gag aag ttc ccc atg			528
Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met			
165	170	175	
gag cgt tgg gtg gcc tgg atg aat ctg tac cgc gtc ttt gtg ggc ttc			576
Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe			
180	185	190	
ctc ttc ccc tgg gca ctc atg ttg ctg tgc tac cgt ggc atc ctg agg			624
Leu Phe Pro Trp Ala Leu Met Leu Leu Cys Tyr Arg Gly Ile Leu Arg			
195	200	205	
gca gtg cag agc agt gtg tcc acc gag cgc cag gag aaa gtc aag atc			672
Ala Val Gln Ser Ser Val Ser Thr Glu Arg Gln Glu Lys Val Lys Ile			
210	215	220	
aaa cgt ctg gcc ctg agc ctc atc gcc att gtg ctg gtg tgc ttt gcg			720
Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala			
225	230	235	240
cct tac cat gct ctc ctg ctg tct cgc agc gcc gtc tac ctg ggc cgg			768
Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg			
245	250	255	
ccc tgg gac tgt ggc ttc gag gag cga gtc ttt tct gcc tac cac agc			816
Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser			
260	265	270	
tcc ctg gcc ttc acc agc ctc aat tgt gtg gct gac ccc atc ctc tac			864
Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr			

275	280	285	
tgc ctg gtc aac gag ggt gcc cgc agt gat gtg gcc aag gcc ctg cac			912
Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His			
290	295	300	
aac ctc ctc cgc ttc ctg gcc agc aac aag ccc cag gag atg gcc aat			960
Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn			
305	310	315	320
gct tcc ctc acc ctg gag aca ccc ttg acc tcc aag agg agc acc acc			1008
Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr			
325	330	335	
ggc aag tcg tcc ggg gct gtc tgg gca gtg cct ccg act gcc cag ggg			1056
Gly Lys Ser Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly			
340	345	350	
gac cag gtg cca ctg aag gtg ctg ctg ccc ccg gca cag tga			1098
Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln			
355	360	365	

<210> 15

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 15

ataagcttgccaccatggacaacagcacgggcac

36

<210> 16

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: synthetic DNA

<400> 16

tagcgccgctcactgtgccgggggcagcag

33

<210> 17

<211> 365

<212> PRT

<213> Rattus norvegicus

<400> 17

Met Asp Asn Ser Thr Gly Thr Trp Glu Gly Cys His Val Asp Ser Arg  
1 5 10 15

Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val  
20 25 30

Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val  
35 40 45

Arg Gln Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala  
50 55 60

Asp Leu Leu Tyr Ile Cys Thr Leu Pro Leu Trp Val Asp Tyr Phe Leu  
65 70 75 80

His His Asp Asn Trp Ile His Gly Pro Gly Ser Cys Lys Leu Phe Gly  
85 90 95

Phe Ile Phe Tyr Ser Asn Ile Tyr Ile Ser Ile Ala Phe Leu Cys Cys  
100 105 110



Ile Ser Val Asp Arg Tyr Leu Ala Val Ala His Pro Leu Arg Phe Ala  
115 120 125

Arg Leu Arg Arg Val Lys Thr Ala Val Ala Val Ser Ser Val Val Trp  
130 135 140

Ala Thr Glu Leu Gly Ala Asn Ser Ala Pro Leu Phe His Asp Glu Leu  
145 150 155 160

Phe Arg Asp Arg Tyr Asn His Thr Phe Cys Phe Glu Lys Phe Pro Met  
165 170 175

Glu Arg Trp Val Ala Trp Met Asn Leu Tyr Arg Val Phe Val Gly Phe  
180 185 190

Leu Phe Pro Trp Ala Leu Met Leu Leu Cys Tyr Arg Gly Ile Leu Arg  
195 200 205

Ala Val Gln Ser Ser Val Ser Thr Glu Arg Gln Glu Lys Val Lys Ile  
210 215 220

Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala  
225 230 235 240

Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg  
245 250 255

Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser  
260 265 270

Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr  
275 280 285

Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His  
290 295 300

Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn  
 305 310 315 320

Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr  
 325 330 335

Gly Lys Thr Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly  
 340 345 350

Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln  
 355 360 365

<210> 18

<211> 1098

<212> DNA

<213> Rattus norvegicus

<400> 18

atg gac aac agc acg ggc acg tgg gag ggc tgc cat gtg gac tct cga 48  
 Met Asp Asn Ser Thr Gly Thr Trp Glu Gly Cys His Val Asp Ser Arg  
 1 5 10 15

gtg gac cac ctc ttc cca cca tcc ctc tac atc ttc gtc atc ggg gtg 96  
 Val Asp His Leu Phe Pro Pro Ser Leu Tyr Ile Phe Val Ile Gly Val  
 20 25 30

ggg ctg ccc acc aac tgc ctg gcc ctg tgg gca gcc tac cgc cag gtg 144  
 Gly Leu Pro Thr Asn Cys Leu Ala Leu Trp Ala Ala Tyr Arg Gln Val  
 35 40 45

cgc cag cgc aat gag ctg ggc gtc tac ctg atg aac ttg agc atc gca 192  
 Arg Gln Arg Asn Glu Leu Gly Val Tyr Leu Met Asn Leu Ser Ile Ala  
 50 55 60

gac ctg ctg tac atc tgt acg ctg ccg ctg tgg gtc gac tac ttc ctc 240

Asp	Leu	Leu	Tyr	Ile	Cys	Thr	Leu	Pro	Leu	Trp	Val	Asp	Tyr	Phe	Leu	
65					70					75					80	
cac	cat	gac	aac	tgg	atc	cac	ggc	ccc	ggc	tcc	tgc	aag	ctc	ttt	ggc	288
His	His	Asp	Asn	Trp	Ile	His	Gly	Pro	Gly	Ser	Cys	Lys	Leu	Phe	Gly	
			85						90					95		
ttc	atc	ttc	tac	agc	aac	atc	tac	atc	agc	atc	gcc	ttc	ctg	tgc	tgc	336
Phe	Ile	Phe	Tyr	Ser	Asn	Ile	Tyr	Ile	Ser	Ile	Ala	Phe	Leu	Cys	Cys	
			100					105					110			
atc	tcc	gtg	gac	cgc	tac	ctg	gct	gtg	gcc	cat	ccg	ctg	cgc	ttt	gcg	384
Ile	Ser	Val	Asp	Arg	Tyr	Leu	Ala	Val	Ala	His	Pro	Leu	Arg	Phe	Ala	
		115					120					125				
cgc	ctg	cgc	cgg	gtc	aag	aca	gca	gta	gct	gtg	agc	tcc	gtg	gtc	tgg	432
Arg	Leu	Arg	Arg	Val	Lys	Thr	Ala	Val	Ala	Val	Ser	Ser	Val	Val	Trp	
	130					135					140					
gcc	acc	gag	cta	ggc	gcc	aac	tgc	gca	ccg	ctc	ttt	cat	gac	gag	ctc	480
Ala	Thr	Glu	Leu	Gly	Ala	Asn	Ser	Ala	Pro	Leu	Phe	His	Asp	Glu	Leu	
145					150					155				160		
ttt	cgt	gat	cgc	tac	aac	cac	acc	ttc	tgc	ttc	gag	aag	ttc	ccc	atg	528
Phe	Arg	Asp	Arg	Tyr	Asn	His	Thr	Phe	Cys	Phe	Glu	Lys	Phe	Pro	Met	
			165					170					175			
gag	cgc	tgg	gtg	gcc	tgg	atg	aac	ctg	tac	cgc	gtc	ttt	gtg	ggg	ttc	576
Glu	Arg	Trp	Val	Ala	Trp	Met	Asn	Leu	Tyr	Arg	Val	Phe	Val	Gly	Phe	
		180					185					190				
ctc	ttc	ccc	tgg	gca	ctc	atg	ttg	ctg	tgc	tac	cgc	ggc	atc	ctg	cgg	624
Leu	Phe	Pro	Trp	Ala	Leu	Met	Leu	Leu	Cys	Tyr	Arg	Gly	Ile	Leu	Arg	
		195					200					205				
gcc	gta	cag	agc	agt	gtg	tcc	acc	gag	cgc	cag	gag	aaa	gtc	aag	atc	672

Ala Val Gln Ser Ser Val Ser Thr Glu Arg Gln Glu Lys Val Lys Ile	
210	220
aaa cgc ctg gcc ctg agc ctc atc gcc atc gtg ctg gtg tgc ttt gca	720
Lys Arg Leu Ala Leu Ser Leu Ile Ala Ile Val Leu Val Cys Phe Ala	
225	240
ccc tac cat gct ctc ttg ctg tct cgc agc gct gtc tat ctg ggc cgg	768
Pro Tyr His Ala Leu Leu Leu Ser Arg Ser Ala Val Tyr Leu Gly Arg	
245	255
ccc tgg gac tgt ggc ttc gag gag cga gtc ttc tct gcc tac cac agc	816
Pro Trp Asp Cys Gly Phe Glu Glu Arg Val Phe Ser Ala Tyr His Ser	
260	270
tcc cta gcc ttc acc agc ctc aat tgc gtg gct gac ccc atc ctc tac	864
Ser Leu Ala Phe Thr Ser Leu Asn Cys Val Ala Asp Pro Ile Leu Tyr	
275	285
tgc ctg gtc aac gag ggt gcc cgt agt gac gtg gcc aaa gcc ctg cac	912
Cys Leu Val Asn Glu Gly Ala Arg Ser Asp Val Ala Lys Ala Leu His	
290	300
aac ctc ctc cgc ttc ctg gcc agc aac aag ccc cag gag atg gcc aat	960
Asn Leu Leu Arg Phe Leu Ala Ser Asn Lys Pro Gln Glu Met Ala Asn	
305	320
gct tcc ctc acc ctg gag aca cca ttg acc tcc aag agg agc acc acc	1008
Ala Ser Leu Thr Leu Glu Thr Pro Leu Thr Ser Lys Arg Ser Thr Thr	
325	335
ggc aaa acg tct ggg gct gtc tgg gca gtg cct ccc act gcc cag ggg	1056
Gly Lys Thr Ser Gly Ala Val Trp Ala Val Pro Pro Thr Ala Gln Gly	
340	350
gac cag gtg cca ctg aag gtg ctg ctg ccc ccg gca cag tga	1098

Asp Gln Val Pro Leu Lys Val Leu Leu Pro Pro Ala Gln  
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<223> Description of Artificial Sequence: synthetic DNA

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20

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: synthetic DNA

<400> 20

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19